#### STIC-Biotech/ChemLib

87940

From: Sent: Schultz, James

Monday, March 03, 2003 11:07 AM

Subject:

STIC-Biotech/ChemLib

sequence search request for 10/003,919

Hello,

I need a length limited nucleotide sequence search performed on SEQ ID NO:3 (5273 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 50 nucleotides. Thank you very much, Doug Schultz

J. Douglas Schultz, Ph.D.
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: / POPS
Phone:
Location:
Date Picked Up:
Date Completed: \3 -12 -03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

/ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

# BioTech-Chem Library Search Results Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact the Bio Tech-Chem searcher who conducted the search or contact:

Mary Hale, Supervisor, 308-4258 CM-1 Room 1E01

Voluntary Results Feedback Form	
> I am an examiner in Workgroup: (Example: 1610)	
> Relevant prior art found, search results used as follows:	•
102 rejection	
103 rejection	<u>.</u>
Cited as being of interest.	· · · · · · · · · · · · · · · · · · ·
Helped examiner better understand the invention.	
Helped examiner better understand the state of the art in their techn	nology.
Types of relevant prior art found:	
Foreign Patent(s)	
Non-Patent Literature (journal articles, conference proceedings, new product announcements et	c.)
> Relevant prior art not found:	
Results verified the lack of relevant prior art (helped determine pate	entability).
Search results were not useful in determining patentability or under	standing the invention.
Other Comments:	

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a
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## ALIGNMENTS

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JOURNAL	REFERENCE	SOURCE	KEYWORDS	ACCESSION	LOCUS DEFINITION	131473/c
webet, J. L. Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same Patent: US 5582979-A 385 10-DEC-1996;	Unclassified.  1 (bases 1 to 44)	Unknown.		I31473 I31473.1 GT:1822264	I31473 44 bp DNA linear PAT 06-FEB-1997 Sequence 385 from patent US 5582979.	
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REFERENCE
AUTHORS
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Sha,N., Walinton,J. and Patel,N.
Gene composition and method
Patent: JP 2000245487-A 601 12-SEP-2000;
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                                                                                BASE COUNT
ORIGIN
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Best Local S
Matches 30
            Query Match 0.6%;
Best Local Similarity 96.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                source
                                                                                                                                                                         I (bases 1 to 31)

I (bases 1 to 31)

Sha, N., Walinton, J. and Patel, N.

Gene composition and method

Patent: JP 2000245487-A 604 12-SEP-2000;

AFIMETRICS INC

OS Unknown

PN JP 2000245487-A/604

PD 12-SEP-2000

PF 27-JAN-2000 JP 2000019392

PF 27-JAN-1999 US 09/238.402

PR 27-JAN-1999 US 09/238.402

PR
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l Similarity 96.8%;
30; Congervative
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Sha,N., Walinton,J. and Patel,N.
Gene composition and method
Patent: JP 2000245487-A 603 12-SEP-2000;
AFIMETRICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD002937.1 GI:18630898
JP 2000245487-A/603.
unidentified.
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JP 2000245487-A/604.
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JP 2000245487-A/603
12-SEP-2000
27-JAN-2000 JP 2000019392
27-JAN-1999 US 09/238.402
NIRA SHA,JANET WALINTON,NIRA PATEL
C12N15/09,C12Q1/68,C12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2938 31 composition and method.
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                                                                                                                                                          /organism-'Unknown'
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10 c 8 g
                                                                                           /organism="unidentified"
/db_xref="taxon:32644"
13 c 6 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"unidentified"
              Score 30.6; DB 6;
Pred. No. 1.1e+05;
1; Mismatches 0;
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Pred. No. 1.1e+05;
1; Mismatches (
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               Gaps
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AUTHORS
TITLE
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BD002940
LOCUS
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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BD002939
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Best Local Similarity
Matches 30; Conserva
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Sha,N., Walinton,J. and Patel,N.
Gene composition and method
Patent: JP 2000245487-A 605 12-SEP-2000;
AFIMETRICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 Gene composition and method. BD002939
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12-SEP-2000
27-JAN-2000 JP 2000019392
27-JAN-1999 US 09/238.402
NIRA SHA, JANET WALINTON, NIRA P
C12N15/09, C12Q1/68, C12N15/00
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milarity 96.8%;
Conservative
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Location/Qualifiers
1. 31
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/db_kref="taxon:32644"
10 c 8 g
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Pred. No. 1
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PAT 31-JAN-2002

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Gaps

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LISTED NO PER ST. P.C. (17.00)

LISSIFIED AA/607.

(bases 1 to 31)

(bases 1 to 31)

(bases 1 to 31)

ACLE

Sha,N., Walinton,J. and Patel,N.

Gene composition and method

JOURNAL

AFHETRICS INC

COMMENT

OS Unknown

PO 12-SEP-2000

PD 12-SEP-2000

PF 27-JAN-2000 JP 20000193°

PR 27-JAN-2000 JP 20000193°

PR 27-JAN-300 JP 20000193°

PR 27-JAN-200 JP 20000193°

PR 87-JAN-200 JP 20000193°

PR 8
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ORIGIN
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BD002941
LOCUS
DEFINITION
                                                                                                                                                          DEFINITION
ACCESSION
VERSION
KEYWORDS
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BD002942
LOCUS
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                                                                        REFERENCE
                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 30
  AUTHORS
TITLE
JOURNAL
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Best Local Similarity
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unclassified.
1 (bases 1 to 31)
Sha,N., Walinton,J. and Patel,N.
Gene composition and method
Patent: JP 2000245487-A 608 12-SEP-2000;
                                                                                                                                                                                                     31
Gene composition and method.
BD002942
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Gene composition and method.
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JP 2000245487-A/608.
unidentified.
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ilarity 96.8%;
Conservative
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Location/Qualifiers
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Location/Qualifiers
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9 c 9 g
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/db_xref="taxon:32644"
9 c 11 g
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Pred. No. 1.1e-
1; Mismatches
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Pred. No. 1.1e+05;
1; Mismatches 0
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AUTHORS
TITLE
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ORIGIN
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KEYWORDS
SOURCE
ORGANISM
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BD002943
                        RESULT 12
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Best Local S
Matches 30
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Sha, N., Walinton, J. and Patel, N.

Sha, N., Walinton, J. and method

Patent: JP 2000245487-A 609 12-SEP-2000;

AFIMERRICS INC

OS Unknown

PN JP 2000245487-A/609

PD 12-SEP-2000

PF 27-JAN-2000 JP 2000019392

PR 27-JAN-1999 US 09/238.402

PR 27-JAN-1999 U
                                                                                                              GCTTTAGCTAAAGTCYCGCGGGTTCCGGCAT 31
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OS Unknown
PN JP 2000245
PD 12-SEP-200
PP 27-JAN-199
PI NIRA SHA, J
PC C12N15/09,
CC Key
FH Key
FT Source
                                                                                                                                                                                                            Similarity 30; Conserv
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JP 2000245487-A/609.
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Gene composition and method.
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    AR178318
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JP 2000245487-A/608
12-SEP-2000
27-JAN-2000 JP 2000013392
27-JAN-1999 US 09/238.402
ATRA SHA, JANET WALLINTOW, NIRA P
C12N15/09,C12Q1/68,C12N15/00
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/db_xref="taxon:32644"
7 c 8 g
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/db_xref="taxon:32644"
8 c 9 g
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REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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AX057285/c
LOCUS
DEFINITION
ACCESSION
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AX323400/c
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FEATURES
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AX057285
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synthetic construct
artificial sequences.
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Sequence 35 from Patent
AX323400
AX323400.1 GI:18094162
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Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B.
Purification of a triple helix formation with an immobilized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
AR178318
                    synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 50)
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Levine, A.J.,
Dorner, F.
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ilarity 76.1%;
Conservative
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Location/Qualifiers
1. .50
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/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
/note="synthetic oligonucleotide"
0 c 25 g 0 t
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0 c 25 g
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          Mitterer, A.,
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Pred. No. 3.1e+05;
0; Mismatches 11;
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WO0192511.
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        Falkner, F.G.,
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YSCMTP032
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Search completed: March 12, Job time: 13185 secs
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AT rich region; GC rich region.
2 of 2
2 of 2
Yeast (Saccharomyces cerevisiae) mitochondrial DNA.
Mitochondrion Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 43)
1 (bases 1 to 43)
1 (bases 1 to 43)
1 Excision sequences in the mitochondrial genome of yeast
Gene 21 (3), 193-202 (1983)
83210931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Targeted angiogenesis
Patent: WO 0075329-A 16 14-DEC-2000;
Edwards Lifesciences Corporation (US) ; Baxter Aktiengesellschaft (AT)
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                                                                                                                                                                                                                                                                        Additional sequences reported in [1], but sequenced in earlier papers, appear in separate entries. Excision repeat corresponds to bases 11 to 33.
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                                                                                                                             Similarity
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/db_xref="taxon:32630"
/note="annealed oligonucleotide"
16 c 27 g 4 t
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                                                                                                                                                                                   /organism="Saccharomyces cerevisiae"
/organelle="mitochondrion"
/organelle="mitochondrion"
/db_xref="taxon:4932"
/db_yref="taxon:4932"
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Pred. No. 1.1e+06;
                                                                                                              Score 25.4; DB 8;
Pred. No. 1.3e+06;
D; Mismatches 6;
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 50
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5273
1 ctagggcatggcatc
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1: /SIDS2/gcgdata/g
2: /SIDS2/gcgdata/g
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11757.215 Million cell updates/sec
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/SIDS2/gcgdata/genesed/genesedn-embl/NA1985.DAT:*
/SIDS2/gcgdata/genesed/genesedn-embl/NA1986.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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AAQ70851	AAQ70852	AAT61246	AAD19288	AAQ33517	AAT47475	AAQ30397	ABN81201	AAH46006	AAH46872	AAS13785	AAS13725	AAQ33543	AAL42352	AAS13774	AAA09913	AAA74333	AAA74332	AAQ33565	AAQ33551	AAT47461	AAQ33523	AAL45123	AAQ33597	AAQ33540	AAX30240	AAS13726	AAD19287	AAX30238	AAQ33577	AAC31611	AAS21107	AAQ33615	AAA79239	AAA79238	AAA79237	
Foldback triplex-f		1body /	•	of micro	triplex	Oligomer LAP322 fo	Litopenaeus vannem	Synthetic oligonuc	B. napus turgor ge	Simple sequence re	Simple sequence re	Microsatellite seq	Novel sand pear mi	$\sim$	:02P2	pine		lite		Foldback triplex f	Sequence of micros		Microsatellite seq	Microsatellite seq	PCR amplification	Simple sequence re	Mammalian IL-12 p4	PCR amplification		Human secreted pro	(GA)25 DNA purific			Human genomic DNA	Human genomic DNA	

#### ALIGNMENTS

RESULT 1

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K P P	X R	X P ?	PA	X PR	XX	X B	×	: × :	2 ×	Z,	X	XX	X	3	X A	XX	TD	AAQ3
Polymorphic bowine DNA markers - used in genetic identification, gene mapping, and selective breeding	WPI; 1992-284684/34.	Georges M, Massey JM;	(GENM-) GENMARK.	15-JAN-1991; 91US-0642342.			MUSALDIUA n.	מאסיייייייייייייייייייייייייייייייייייי	פודווע לייניים ליינים לייניים לייניים ליינים ל	genetic mapping; traits; amplification; ss.	PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;	Microsatellite sequence from clone AGLAZB5.		02-FEB-1993 (first entry)	AAQ33591;		AAQ33591 standard; DNA; 49 BP.	AAQ33591/c

**Fable** 

7; Page 165;

517pp;

English.

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RESULT 2
AAT65793/c
ID AAT65793;
XX AAT65793;
XX AAT65793;
XX AAT65793;
XX Polymorphism; repeat sequence from polym KW PCR; polymerase chain reac KW linkage analysis; genetic KW hybridisation; chromosome; XX PN US5582979-A.
XX US5582979-A.
XX US5582979-A.
XX PN US5582979-A.
XX US558297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
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See also AAQ33501-34437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease,
                                                                                                                                                                                                                                                 Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as
                                                                                                                                                                                         Disclosure; Column 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49
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89US-0341562.
94US-0222177.
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Pred. No. 8
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The present invention describes a nucleic acid segment of 10-100 CC contiguous bases chosen from one of 632 fragments (AAA78631 to AAA79262), where the segment comprises a polymorphic site or an CC immediately adjacent base, or the complement of the segment. Also CC described are: (1) an allele-specific oligonuclectide that hybridises to CC a segment of the novelty; (2) an isolated nucleic acid comprising a CC sequence of the novelty where the polymorphic site within the sequence is cocupied by a base other than the reference base indicated in the CC specification; and (3) analysing a nucleic acid, comprising obtaining a CC nucleic acid from an individual, and determining a base occupying any one CC of the polymorphic sites of the novelty. The nucleic acid segments and CC method can be used to analyse an individuals nucleic acid segments and CC the presence of polymorphisms. The method can also be used to test for a CC disease phenotype and correlate the presence of the phenotype with a CC particular polymorphism. The presence of polymorphic sites are useful CC for, e.g. forensics, paternity testing, correlation of polymorphisms.
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AAA79230
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Best Local
                                                                                                                                                                                                                                                                                                                                                                             Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics,
                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                    paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(GC-dA), (GG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf122 which contains the repeat sequence having the formula: TTTACAGTAG(CA)17
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-500198/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-1999;
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hybridisation; polymorphic site; forensic; paternity testin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                    Page 22;
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Pred. No. 9
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                                                   The present invention describes a nucleic acid segment of 10-100 CC contiguous bases chosen from one of 632 fragments (AAA78631 to CAAA79262), where the segment comprises a polymorphic site or an CC immediately adjacent base, or the complement of the segment. Also CC described are: (1) an allele-specific cligonucleotide that hybridises to CC estimated are: (1) an allele-specific cligonucleotide that hybridises to CC experiment of the novelty where the polymorphic site within the sequence is CC occupied by a base other than the reference base indicated in the Specification; and (3) analysing a nucleic acid, comprising obtaining a complication; and (3) analysing a nucleic acid, comprising obtaining a complication; and (3) analysing a nucleic acid, comprising obtaining a complication of the polymorphic sites of the novelty. The nucleic acid segments and CC mathod can be used to analyse an individuals nucleic acid segments for CC the presence of polymorphisms. The method can also be used to test for a CC disease phenotype and correlate the presence of the phenotype with a CC disease phenotype and correlate the presence of the phenotype with a CC particular polymorphism. The presence of polymorphisms of the phenotype with a CC disease phenotype traits and for genetic mapping of phenotypic traits. CC With phenotypic traits and for genetic mapping of phenotypic traits. CC CAA786531 to AAA79262 represent sequence tags of human genomic DNA CC polymorphic site is indicated using IUPAC-IUB nomenclature.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics,
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   Sequence 31 BP;
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Pred. No. 9.1e+02
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Query Match Best Local Matches

Similarity

96.8%; C;

Score 30.6; DB 21; Pred. No. 9.1e+02; 1; Mismatches 0;

Length Indels

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RESULT
CC ontiguous bases chosen from one of 632 fragments (AAA78631 to CC contiguous bases chosen from one of 632 fragments (AAA78631 to CC AAA79262), where the segment comprises a polymorphic site or an CC immediately adjacent base, or the complement of the segment. Also CC described are: (1) an allele specific oligonucleotide that hybridses to CC assyment of the novelty; (2) an isolated nucleic acid comprising a CC occupied by a base other than the reference base indicated in the Specification; and (3) analysing a nucleic acid, comprising obtaining a CC nucleic acid from an individual, and determining a base occupying any one CC of the polymorphic sites of the novelty. The nucleic acid segments and CC method can be used to analyse an individuals nucleic acid segments and CC method can be used to analyse an individuals nucleic acid segments and CC disease phenotype and correlate the presence of the phenotype with a CC disease phenotype and correlate the presence of the phenotype with a CC disease phenotype traits and for genetic mapping of phenotypic traits. CC with phenotypic traits and for genetic mapping of phenotypic traits. CC AAA78631 to AAA79262 represent sequence tags of human genomic DNA CC polymorphic site is indicated using TUPAC-TUB nomenclature.
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30; Conservative
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                                                                                                                                 Similarity
30; Conser
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                                                                                                                                                                  0.6%;
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                                                                                                                                                                  Pred.
                                                                                                                                                                         Score 30.6;
Pred. No. 9
                                                                                                                                     Mismatches
                                                                                                                                                                         1e+02
                                                                                                                                                                                                      DB 21;
                                                                                                                                     0
                                                                                                                                     Indels
                                                                                                                                                                                                      Length
                                                                                                                                                                                                         31;
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RESULT 8
AAA79235
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                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                    Matches
                                                                                                                 3999 AACACCGAGCTCCCGCATCACGGCAAGCACC 4029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genomic DNA polymorphic site sequence tag
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AAA79235 standard; DNA;
                                                                                                                                                                                                                    Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    paternity testing, genetic mapping,
                                                                                                                                                               Local
                                                                                   AACACCGAGCTCCCGYATCACGGCAAGCACC
                                                                                                   l Similarity
30; Conserv
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                                                                                                                                                                                                                    BP;
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                                                                                                                                                    Conservative
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                                                                                                                                                                                                                    9 A; 13 C; 6 G;
                                                                                                                                                                 96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymorphic
 31
                                                                                                                                                                 Score 30.6;
Pred. No. 9.
                                                                                                                                                                                                                    2 T; 1 other;
                                                                                                                                                    Mismatches
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RESULT 9
AAA79236
ID AAA7
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AC AAAA7
AC AAAA7
DT 20-1
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DT 40-1
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                                                                                                                                                                                                                                                                                                                                                                              CC ontiguous bases chosen from one of 632 fragments (AAA78631 to CAAA79262), where the segment comprises a polymorphic site or an CC immediately adjacent base, or the complement of the segment. Also CC described are: (1) an allele-specific oligonuclectide that hybridises to CC described are: (1) an allele-specific oligonuclectide that hybridises to CC segment of the novelty; (2) an isolated nucleic acid comprising a CC occupied by a base other than the reference base indicated in the specification; and (3) analysing a nucleic acid, comprising obtaining a cC nucleic acid from an individual, and determining a base occupying any one CC in the polymorphic sites of the novelty. The nucleic acid segments and CC method can be used to analyse an individuals nucleic acid segments and CC the presence of polymorphisms. The method can also be used to test for a CC disease phenotype and correlate the presence of the phenotype with a CC disease phenotype and correlate the presence of the phenotype with a CC disease phenotype and correlate the presence of polymorphisms. The presence of polymorphisms is paternity testing, correlation of polymorphisms. CC with phenotypic traits and for genetic mapping of phenotypic traits. CC AAA78631 to AAA79262 represent sequence tags of human genomic DNA CC fragments containing polymorphic sites. The base occupying the CC plymorphic site is indicated using IUPAC-IUB nomenclature.
                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                           Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity testing, genetic mapping,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 22; 141pp; English.
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                                                                                                                                                                                                                                                                                                                                                  Sequence 31
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                Human genomic DNA polymorphic site sequence tag SEQ II) NO:606
                                                  20-NOV-2000
                                                                                                                       AAA79236 standard;
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                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                  30;
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                                                  (first entry)
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                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                               96.8%;
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pred. No. 9.1e+02;
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Best Local S
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                                Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe; hybridisation; polymorphic site; forensic; paternity testing; medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
                                                                                                                                                                                         AAA79237;
                                                                                                                                                                                                                                                                                                                                                              4310 TCTGGGTCCCCAGCTCGCTCTTGGTACTTGG 4340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity testing, genetic mapping,
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                                                                                                              Human genomic
                                                                                                                                                    20-NOV-2000
                                                                                                                                                                                                                              AAA79237 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31 BP; 2 A;
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                                                                                                              DNA polymorphic
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30.6; DB 21; Pred. No. 9.1e+02;
                                                                                                                site
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Matches
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                                              02-AUG-2000
                                                                                                      EP1024200-A2
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                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Human genomic DNA polymorphic site sequence
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30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 11 G; 6 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>بر</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30.6; DB 2:
Pred. No. 9.1e+02
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   632 fragments (AAA78631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                   tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                   Ħ
                                                                                                                                                                                                                      mapping;
                                                                                                                                                                                                                                                                                                                                                      NO:608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 10-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
ACC CANADA CANAD
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Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe; hybridisation; polymorphic site; forensic; paternity testin medicine; phenotypic trait; genetic analysis; genetic mapping; ds.

Human genomic

DNA

polymorphic site

sequence

tag

SEQ

B

NO:609

0

testing;

(AFFY-) AFFYMETRIX INC

27-JAN-1999; 26-JAN-2000; 02-AUG-2000 EP1024200-A2 Homo sapiens.

9905-0238402

2000EP-0250023

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QΥ
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                                                                                                                  AAA79239
                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                      CC configuous bases chosen from one of 632 fragments (AAA78631 to AAA78632), where the segment comprises a polymorphic site or an CC immediately adjacent base, or the complement of the segment. Also CC described are: (1) an allele-specific oligonucleotide that hybridises to CC segment of the novelty; (2) an isolated nucleic acid comprising a CC sequence of the novelty where the polymorphic site within the sequence is CC occupied by a base other than the reference base indicated in the CC occupied by a base other than the reference base indicated in the controlled by a base other than the reference base indicated in the controlled by a base other than the reference base indicated in the controlled by a base other than the reference base indicated in the controlled by a base other than the reference base indicated in the controlled by a base occupying any one CC indicated from an individual, and determining a base occupying any one CC indicated from an individual, and determining a base occupying any one CC interpolation of polymorphisms. The method can also be used to test for a CC interpolation of polymorphisms. The method can also be used to test for a CC interpolation of polymorphisms. The method can also be used to test for a controlled polymorphism. The presence of polymorphic sites are useful CC in presence, paternity testing, correlation of polymorphisms CC with phenotypic traits and for genetic mapping of phenotypic traits.

CC AAA78631 to AAA79562 represent sequence tags of human genomic DNA CC polymorphic site is indicated using TUPAC-TUB nomenclature.
                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 30
                                                                                                                                                                                                      AAA79239 standard; DNA; 31 BP
20-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a nucleic acid segment of 10-100 contiguous bases chosen from one of 632 fragments (AAA78631 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 22; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-2000; 2000EP-0250023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic polymorphic nucleic acid segments, allele specific rs and probes, and methods of analysis, useful for e.g. forensics,
                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shah N, Warrigton
                                                                                                                                                                                                                                                                                                                                                                                       BP; 7 A; 7 C; 8 G; 8 T; 1 other;
                                                                                                                                                                                                                                                                                                   Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                       0.6%;
                                                                                                                                                                                                                                                                                                                       Score 30.6; DB
Pred. No. 9.1e+
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                         .1e+02
                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                 ç,
                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                               Gaps
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configuous bases chosen from one of 522 fragments (AAA79561 to AAA79262), where the segment comprises a polymorphic site or an immediately adjacent base, or the complement of the segment. Also compared to the segment of the segment of the segment of the novelty; (2) an isolated nucleic acid comprising a segment of the novelty where the polymorphic site within the sequence is occupied by a base other than the reference base indicated in the specification; and (3) analysing a nucleic acid, comprising obtaining a nucleic acid sequence is occupied by a base other than the reference base indicated in the paper of the polymorphic sites of the novelty. The nucleic acid segments and comprise and contained an individual, and determining a base occupying any one of the polymorphic sites of the novelty. The nucleic acid segments and method can be used to analyse an individuals nucleic acid segments and compared the presence of polymorphisms. The method can also be used to test for a disease phenotype and correlate the presence of the phenotype with a contained polymorphism. The presence of polymorphism is paternity testing, correlation of polymorphisms of the phenotypic traits and for genetic mapping of phenotypic traits. CC AAA78631 to AAA79262 represent sequence tags of human genomic DNA corporations of the presence containing polymorphic sites. The base occupying the polymorphic site is indicated using IUPAC-IUB nomenciature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4722 GCTTTAGCTAAAGTCCCGCGGGTTCCGGCAT 4752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                               PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                             Microsatellite sequence from clone AGLA33.
                                                                                                                                                                                                                                                                                                                                                         02-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           AAQ33615;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ33615 standard; DNA; 48 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31 BP; 5 A; 8 C; 9 G; 8 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a nucleic acid segment of 10-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 22; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patil N,
   Polymorphic bovine DNA markers -
                                                                                            (GENM-) GENMARK.
                                                                                                                                                                                      06-AUG-1992
                                                                                                                                                                                                                    W09213102-A.
                                                                                                                                                                                                                                                    Bos taurus
                                 WPI; 1992-284684/34.
                                                                Georges M,
                                                                                                                         15-JAN-1991;
                                                                                                                                                         15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTTTAGCTAAAGTCYCGCGGGTTCCGGCAT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shah N, Warrigton JA;
                                                            Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                           91US-0642342
                                                                                                                                                       92WO-US00340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30.6; DB 21
Pred. No. 9.1e+02;
used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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AAS21107/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
             Purifying double-stranded (ds) DNA from a solution containing dsDNA and other components, comprises passing the solution through a support comprising a coval-ently coupled oligonucleotide able to form a triple helix with the dsDNA.
                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                       Crouzet J,
                                                                                                                                                                                                                                                 06-DEC-2001
                                                                                                                                                                                                                                                                                                                                          repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS21107;
                                                                                                                                                                                                                                                                             WO200192511-A2
                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local 5;
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The sequence is that of a bovine microsatellite sequence obtd. by correcting a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol Sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, CC Oligonia Distribution of microsatellites in the bovine genome is estimated at >100, CC Oligonia Distribution and indexed herein (see below). The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). CC The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program CC optiprim). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait traits esp. in cattle, to allow selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; DNA purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS21107 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48 BP; 24 A; 0 C; 24 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Table 7; Page 175; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene mapping, and selective breeding
WPI; 2002-097772/13.
                                                                                                                                                                                                               25-MAY-2001; 2001WO-US17122
                                                                                                      (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                           26-MAY-2000; 2000US-0580923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GA)25 DNA purification oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 CCCCCCCTCTCTCTCTTTCTCTCTCTCTCTCTCTTGCTTTGCTTTCTGT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                 Scherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_type- "TANDEM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                             'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%;
                                                 Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               triple helix; plasmid purification
                                                                                                                                                                                                                                                                                                                                                                          "GA repeat type"
                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                 Wils P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28.4; DB 13;
Pred. No. 3.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                    Blanche
                                                 '3
                                                    Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                 œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 15
AAC31611/c
ID AAC31611;
XX
AC31611;
XX
DT 06-OCT-2000 (first entry)
XX
Human secreted protein 5' EST,
XX
DE Human; 5' EST; expressed seque
XW gene therapy; chromosome mappi
XX
Homo sapiens.
XX
PN EP1033401-A2.
PN EP1033401-A2.
XX
O6-SEP-2000; 2000EP-0200610.
XX
C6-FEB-1999; 99US-0122487.
XX
PN (GEST) GENSET.
XX
VPI; 2000-500381/45.
XX
PN wpi; 2000-500381/45.
XX
VPI obtaining cDNAs and genomic DN
PT diagnostic, forensic, gene the
XX
Claim 1; SEQ ID 35686; 71pp +
XX
CC Inhanan RNAs or polyA+ RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention comprises a method of purifying double-stranded DNA from CC a solution containing the double-stranded DNA mixed with other components, comprising passing the solution through a support components, comprising passing the solution through a support comprising CC with the double-stranded DNA by hybridisation with a specific sequence present in the double-stranded DNA. The method is useful for purifying CC double-stranded DNA contained in a solution and mixed with other CC components. The new method is a simple, rapid and effective method for CC purification, and makes it possible to obtain especially high CC purifies with high yields. The method enables DNA to be purified from CC complex mixtures comprising other nucleic acids, proteins, endotoxins, cucleases and the like. The supports may be readily recycled, and the CC DNAs obtained display improved properties to pharmaceutical safety. CR Purther, the method entails only one step contrary to prior art. CC Purther, the sequence represents a DNA sequence contained within the CC plasmid pXL2726. This sequence is used for purification of this passing using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
            The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTRA) of the mRNA because they are often obtained from oilgo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 35686; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein 5' EST, SEQ ID NO: 35686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50 BP; 25 A; 0 C; 25 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 CCCCCCCTCTCTCTCTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Page 20; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%;
76.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28.4;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .8e+03
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Best Local
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                                                                                                                                                                      derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intert 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                         Sequence 50 BP; 21 A; 4 C; 19 G; 3 T; 3 other;
                                                                                                                                                        expression and secretion vectors.
Similarity
                                                             Conservative
                                                                           0.5%;
81.1%;
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                                                                           Score 28.2; DB 21
Pred. No. 4.3e+03;
                                                               Mismatches
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                                                                                          21;
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Search completed: March 11, Job time : 1015 secs 2003, 21:11:19

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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5273
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/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/6B_COMB.seq:*
/cgn2_6/ptodata/1/lna/6B_COMB.seq:*
/cgn2_6/ptodata/1/lna/backfiles1.seq:*
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                         US-08-22-177A-385
US-09-580-923-358-10
US-08-933-358-10
US-09-641-638-934
US-09-641-638-934
US-09-641-638-934
US-09-641-638-93-46
US-09-281-481A-2
US-09-281-481A-2
US-09-281-481A-2
US-09-281-181-23A-14
US-09-281-181-123A-14
US-08-418-123A-13
US-08-418-123A-11
US-08-418-123A-11
US-08-418-123A-11
US-08-418-123A-11
US-08-418-123A-11
US-08-418-123A-10
US-08-418-123A-10
US-08-418-123A-7
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Sequence 385, Appli Sequence 18, Appli Sequence 934, Appli Sequence 935, Appli Sequence 22, Appli Sequence 28, Appli Sequence 28, Appli Sequence 215, Appli Sequence 15, Appli Sequence 17, Appli Sequence 11, Appli Sequence 12, Appli Sequence 11, Appli Sequence 10, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 19, Appli Sequence 3, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 3, Appli Sequence 11, Appli Sequence 3, Appli Sequence 11, Appli Sequence 12, Appli Sequence 23, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 1
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US-08-222-177A-385/c
     Query Match 0.6%;
Best Local Similarity 83.3%;
Matches 35; Conservative
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22.4 0.4 24 US-09-235-614-8 22.4 0.4 24 US-09-235-614-9 22.4 0.4 24 US-09-235-614-10 22.4 0.4 24 US-09-235-614-11 22.4 0.4 24 US-09-235-614-11 22.4 0.4 24 US-09-487-130-1 22.4 0.4 24 US-09-487-130-2 22.4 0.4 24 US-09-487-130-2 22.4 0.4 24 US-09-487-130-4 22.4 0.4 24 US-09-487-130-5 22.4 0.4 24 US-09-487-130-5 22.4 0.4 24 US-09-487-130-5 22.4 0.4 23 US-08-487-130-5 22.4 0.4 33 US-08-068-747-7	222222222222222222222222222222222222222	0 0 4 4 4 4 8 4 70		C 34 C 35 C 37	C 31 30	c c
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8, Appli 9, Appli 10, Appl 11, Appli 1, Appli 2, Appli 2, Appli 3, Appli 4, Appli 4, Appli		7, Appli	Tddv	App1 App1	) App. 1991	Appl:

#### US-08-222-177A-385 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 44 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomi IMMEDIATE SOURCE: CLONE: mfd122rs COUNTRY: USA ZIP: 53717-1914 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/222,177A FILING DATE: 21-APR.1989 ATTORNEY/AGENT INFORMATION: NAME: SATA, Charles S. REFERENCE/DOCKET NUMBER: 09865.601 TELECOMMUNICATION INFORMATION: Sequence 385, Application US/08222177A Patent No. 5582979 GENERAL INFORMATION: APPLICANT: Weber, James L. TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS NUMBER OF SEQUENCES: 460 CORRESPONDENCE ADDRESS: ADDRESSEE: DeWitt STREET: 8000 Excel CITY: Madison STATE: Wisconsin TELEFAX: (608) 831-2106 E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401 DNA (genomic) OF USING SAME

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0; Mismatches Score 30.8; Pred. No. 65;

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Length 44; Indels

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Gaps

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GENERAL INFORMATION:
APPLICANT: Day, Peter C.
APPLICANT: Liu, Debang
TITLE OF INVENTION: DNA BRACKETING LOCUS COMPATIBLE STANDARDS FOR
TITLE OF INVENTION: ELECTROPHORESIS
FILE REFERENCE: 434001aa
CURRENT APPLICATION NUMBER: US/08/933,358
CURRENT FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:PRIMER SEQUENCE
US-08-933-358-18
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Best Local S
Matches 35
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SEO ID NO 35
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                     Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35, Application US/09580923
Patent No. 6319672
                                                                                     Query Match
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/FR95/01468
PRIOR FILING DATE: 1995-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE FILE REFERENCE: 03804.0138-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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272 CTCTCTCTTCTCTCTCTCTCTCTCTTGCTTGGTTTCTGTAATGAG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 76.1 nes 35; Conservative
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Wils, Pierre
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                                                       Conservative
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 Mismatches

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                                                                    Score 28;
Pred. No.
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Pred. No. 2.9e+02;
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                                                                  .6e+02;
                                                     10; Indels
                                                                                     Length 47;
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271 TCTCTCTTTCTCTCTCTCTCTTGCTTGGTTT 305

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US-09-641-638-934/c
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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Debang
APPLICANT: Liu, Debang
TITLE OF INVENTION: DLA BRACKETING LOCUS COMPATIBLE STANDARDS FOR
TITLE OF INVENTION: ELECTROPHORESIS
FILE REFERENCE: 434001aa
CURRENT FILING DATE: 1997-09-18
CURRENT FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 20
LENGTH: 48
TYPE: DAA
                                                                                                                                                                                                                             SEQ ID NO 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
Matches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                         NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-836-237 : polymorphic base A
                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                    FEATURE:
                                                                                                                                                                    ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: PRIMER SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 CCCCTCTCTCTCTCTCTCTCTCTTGCTTGGTTTCTGTAAT 312
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                    Local
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o. 6432648
                  0.5%;
Similarity 80.0%;
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34; Conservative
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  Conservative
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                  Score 25; DB 4;
Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26.8; DB 3;
Pred. No. 7.4e+02;
0; Mismatches 12;
                                  Length 47;
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  Indels
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.5
Best Local Similarity 80.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-641-638-935/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENEST .051Cpl CURRENT APPLICATION NUMBER: US/09/641,638 CURRENT APPLICATION NUMBER: US/09/502,330 PRIOR APPLICATION NUMBER: US 09/502,330 PRIOR FILING DATE: 2000-02-11 PRIOR APPLICATION NUMBER: US 60/133,200 PRIOR PILING DATE: 1999-05-07 PRIOR FILING DATE: 1999-05-07 PRIOR FILING DATE: 1999-05-07 PRIOR FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-281-481A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: allele
LOCATION: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: DAWKINS, ROGER L. and ABRAHAM, Lawrence J.
TITLE OF INVENTION: GENETIC ANALYSIS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENCTH:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 TCTCTCTTTTCTCTCTCTCTCTCTCTTGCTTGGTTT 305
                                                                                                                                                                                                                                                   ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY
STATE: NEW YORK
                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 TCTCTCTCTCTCTCTCWTTCGCTCGCTTGCTCT 8
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                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
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                                                                           US/09/281,481A
  US/08/893,971
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Pred. No. 2.1e
1; Mismatches
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2.1e+03;
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US-09-281-481A-2
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Best Local Similarity 92.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: +516 742 4366
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                 APPLICATION NUMBER: US/08/893,971
FILING DATE: 16-JUL-1997
APPLICATION NUMBER: US 232,229
FILING DATE: 29-ARR-1994
APPLICATION NUMBER: PK9279 (AU)
APPLICATION NUMBER: PC17AU92/00583
FILING DATE: 01-NOV-1991
APPLICATION NUMBER: PC17AU92/00583
FILING DATE: 30-OCT-1992
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-JUL-1997
APPLICATION NUMBER: US 232
FILING DATE: 29-APR-1994
APPLICATION NUMBER: PK9279
FILING DATE: 01-NOV-1991
APPLICATION NUMBER: PCT/AN
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
                                       TELEFAX: +516 742 4366 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DIGIGLIO, FRANK S
REFERENCE, DOCKET NUMBER: 92'
TELECOMMUNICATION INFORMATION:
TELEPHONE: +516 742 4343
                                                                       NAME DIGIGLIO, FRANK S
REFERENCE/POCKET NUMBER: 92
TELECOMMUNICATION: INFORMATION:
TELEPHONE: +516 742 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 CCCTCTCTCTCTTCTCTCTCTCTCT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UNITED STATES OF AMERICA ZIP: 11530-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SCULLY SCOTT MURPHY 6 PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/281,481A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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Pred. No. 1.9e+03
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; TYPE: nucleic acid
; STRANDEDNESS: sing,
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-469-802B-28
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                                RESULT 10
US-08-267-803B-46/c
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 26; Conserv
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TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
Sequence 46, Application US/08267803B Patent No. 5834183
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 31,977
REFERENCE/TOKET NUMBER: 110.00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1217
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANUXESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                    31 CTCTCTCTCTCTCTCTCTCTCTCATTCT 2
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o. 5741645
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96.2%;
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Pred. No. 4.1e+03;
0; Mismatches 4;
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Pred. No. 2.3e+03;
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US-08-418-123A-15

; Sequence 15, Application US/08418123A
; Patent No. 5739308
; GENERAL INFORMATION:
; APPLICANT: Kandimalla, Ekambar R.
APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: Integrated Olig
; NUMBER OF SEQUENCES: 23
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APPLICANT: Chung, Ming-yi
APPLICANT: Chung, Ming-yi
APPLICANT: Coghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4%;
Best Local Similarity 86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 46:
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APPLICANT: Orr, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/267,803B FILING DATE: 28-UW-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 7.0 for Windows
CURRENT APPLICATION DATA:
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS.
ADDRESSES: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 CTCTCTCTCTCTCTCTCTCTCTCTCTCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box CITY: Minneapolis STATE: MN
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APPLICATION NUMBER:
                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                             60606
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                                                                                                                                                                                                                                                                                                          Integrated Oligonucleotides
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US/08/418,123A
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Pred. No. 4
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US-08-418-123A-15
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Best Local Similarity 81.8%;
Matches 27; Conservative
Query Match
                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greenfleld, Michael S.
REGISTRATION NUMBER: 37.142
REFERENCE/DOCKET NUMBER: 93,000-E
TELECOMUNICATION INFORMATION:
312.7715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5739308
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 7.0 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,123A
FILING DATE: APII 6, 1995
CLASSIFICATION. 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kandimalla, Ekambar K.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Integrated Oligonucleotides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
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                                              HYPOTHETICAL: N
ANTI-SENSE: YES
                                                                          MOLECULE TYPE:
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CITY: Chicago
STATE: Illinois
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REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 93,000-E
                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                        TELEPHONE: 312/715-1234
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                                                                                              TOPOLOGY:
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                                                                           DNA (genomic)
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 0.4%; Score 23.4;
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Pred. No. 4.7e
0; Mismatches
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4.7e+03;
 DB 1;
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Length 35;
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RESULT 14
US-08-418-123A-12
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                                                                                                                                Sequence 12, Application US/08418123A Patent No. 5739308
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 7.0 for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,123A
FILING DATE: April 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
                                                            GENERAL INFORMATION:
APPLICANT: Kandimalla, Ekambar R.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Integrated Oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNJ
HYPOTHETICAL: NO
ANTI-SENSE: YES
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REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDINESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kandimalla, Ekambar R
APPLICANT: Agrawal, Sudhir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                   TYPE: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
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300 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                  0.4%;
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Pred. No. 4.9e+03;
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US-08-418-123A-11
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 7.0 for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,123A
FILING DATE: April 6, 1995
CLASSIFICATION: S36
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 93,000-E
TELECOMBUNICATION INFORMATION:
TELECOMBUNICATION INFORMATION:
TELECOMBUNICATION INFORMATION:
TELECOMBUNICATION INFORMATION:
TELECOMBUNICATION INFORMATION:
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Best Local 9
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                                                 APPLICATION NUMBER: US/08/418,123A
FILING DATE: April 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REPERENCE/DOCKET NUMBER: 37,142
REPERENCE/TOKET NUMBER: 93,000-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
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TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 12:
                    TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 7.0 for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 STREET: 300 South
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHEFICAL: NO ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kandimalla, Ekambar R.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Integrated Oligonucleotides
NUMBER OF SEQUENCES: 23
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 CCCCCCCCTCTCTCTCTTCTCTCTCTCTCTCT 295
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COUNTRY: U.S.A.
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81.8%;
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Pred. No. 4.9e+03;
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                                                                                  MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-418-123A-11
                    γ
                                        Query Match
Best Local Similarity
Matches 27; Conserv
            LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                            TOPOLOGY: linear
N
 CGCACCCATCTCTCTCCTCTCTCTCTCTCTCT
                                          Conservative
                                                                                                                  DNA (genomic)
                                                    0.4%;
81.8%;
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                                                    Score 23.4; DB Pred. No. 5e+03;
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Search completed: March 12, 2003, 02:53:00 Job time: 171 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
              200.000 D11.0000 B20.0000 D12.0000 D12.
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seq length:
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            /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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10 US-09-263-959-766
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10 US-09-263-959-538
10 US-09-740-002-4
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10 US-09-740-002-1
10 US-09-740-002-1
10 US-09-988-899-55
10 US-09-888-899-55
10 US-09-863-526-27
10 US-09-863-526-27
10 US-09-863-526-27
10 US-09-863-526-27
10 US-09-963-526-27
10 US-09-740-002-3
10 US-09-740-002-3
10 US-09-740-002-5
10 US-09-965-925-92-12
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10 US-09-965-956-6
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Sequence 765, Appli
Sequence 474, App
Sequence 474, App
Sequence 47, Appli
Sequence 27, Appli
Sequence 17, Appli
Sequence 55, Appli
Sequence 272, Appli
Sequence 272, Appli
Sequence 273, Appli
Sequence 44, Appli
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Sequence 12, Appli
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ACCAGCA        AGCCGCC	itch Sal Simi 33;	GENERAL INFORMATION: APPLICANT: Mitterer APPLICANT: Mitterer APPLICANT: Scheifli APPLICANT: Scheifli APPLICANT: Edwards TITLE OF INVENTION: FILE REFERENCE: 2055 CUGRENT APPLICATION CURRENT FILING DATE: 1 PRIOR APPLICATION NUL PRIOR APPLICATION NUL PRIOR FILING DATE: 1 PRIOR APPLICATION NUL PRIOR APPLICATION NUL PRIOR FILING DATE: 1 PRIOR APPLICATION NUL PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 PRIOR APPLICATION NUL PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 PRIOR APPLICATION NUL PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 PRIOR APPLICATION NUL PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 PRIOR APPLICATION NUL PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 PRIOR APPLICATION NUL PRIOR FILING DATE: 2 NUMBER OF SEO 1D NOS SOFTWARE: PATENTIN IN SEQ ID NO 16 LENGTH: 50 TYPE: DNA ORGANISM: ATTIFICIAL OTHER INFORMATION: 1 OTHER INFORMATION: 1	-650-16 e 16, A	20.2 20.2 20.2 20.2 20.2 20.2 20.2 20.2
AGACCCCG	h 0. Similarity 73. 33; Conservative	GENERAL INFORMATION:  APPLICANT: Levine, Arnuld J.  APPLICANT: Levine, Arnuld J.  APPLICANT: Mitterer, Artur  APPLICANT: Falkner, Falko-Guenter  APPLICANT: Falkner, Friedrich  APPLICANT: Scheiflinger, Friedrich  APPLICANT: Scheiflinger, Friedrich  APPLICANT: Borner, Friedrich  APPLICANT: Borner, Friedrich  APPLICANT: Scheiflinger, Friedrich  APPLICANT: NUMER: US(99)  CURRENT APPLICATION NUMBER: US (99/32)  PRIOR APPLICATION NUMBER: US (99/32)  PRIOR FILING DATE: 1999-06-01  PRIOR APPLICATION NUMBER: US (99/32)  PRIOR APPLICATION NUMBER: US (99/32)  PRIOR APPLICATION NUMBER: US (99/32)  PRIOR FILING DATE: 2000-05-31  NUMBER OF SEQ ID NOS: 24  SOFTWARE: PATENTIN VET. 2.1  SEQ ID NO 16  LENGTH: 50  TYPE: DNA  ORGANISM: Artificial Sequence  FEATURE:  OTHER INFORMATION: Description of  OTHER INFORMATION: Oligonucleotid  S-09-782-650-16	2-650-16/c 2-650-16/c 2-650-16/c 2-650-16/cation US	
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ACCAGCAGACCCCGCCCACCCGGACGCCGCGGCGCCGCTGCCAG	Score 25.8; DB 10; L4 Pred. No. 1.6e+03; 0; M1smatches 12; I1	h orporation genesis 782,650 4,079 7,045 /14988	ALIGNMENTS /09782650	0 US-09-740-002-10 US-09-864-785-129 US-09-864-785-1279 US-09-864-785-1279 US-09-864-785-1279 US-09-863-806-120 US-09-91-484A-195 US-09-91-484A-195 US-09-91-484A-195 US-09-91-484A-195 US-09-91-484A-195 US-09-91-484A-195 US-09-91-2-63-13 US-09-912-2-63-215 US-09-912-2-63-215 US-09-912-2-83-193 US-09-907-844-193 US-09-907-844-193 US-09-906-838-193 US-09-906-742-193 US-09-906-742-193 US-09-906-838-193 US-09-908-83-193 US-09-908-808-808
3942	Length 50; Indels 0; Gaps 0	Sequence : annea Led		Sequence 10, Appli Sequence 9, Appli Sequence 1,79, Ap Sequence 127, Appli Sequence 15, Appli Sequence 15, Appli Sequence 13, Appli Sequence 193, Appli S
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; OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-6
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                                                                                SOFTWARE: PatentIn version 3.0 
)EQ ID NO 6
LENGTH: 27
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TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/735,363A CURRENT FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                              APPLICANT: Filion, Mario APPLICANT: Phillip, Nigo
                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/170,325 PRIOR FILING DATE: 1999-12-13
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                                                                                                                                        NUMBER OF SEQ ID NOS: 87
                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/228,925
PRIOR FILING DATE: 2000-08-29
                                ORGANISM: Artificial Sequence FEATURE:
                                                                    TYPE: DNA
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REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 05-MAR-199
CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
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LENGTH: 37 base pairs
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STREET: Seattle
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 98104-7092
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Local Similarity 87.5%;
es 28; Conservation
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Pred. No. 1.4e+03;
0; Mismatches 4;
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US-09-740-002-4/c
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GENERAL INFORMATION:

APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
APPLICANT: MORROW, PHILLIP
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: MEDITRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIHODIES
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
FILE REFERENCE: 037003-0275759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. US20020150891A1 GENERAL INFORMATION:
                                                                                                                                                                           Sequence 4, Application US/09740002 Patent No. US2002001798A1
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CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: McMasters, David D.
REGISTRATION NUMBER: 33,9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/263,959 FILING DATE: 05-MAR-1999
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Similarity 96.2%;
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Koop, Ben F.
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Pred. No. 2.
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Pred. No. 2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION: OMAR-1999
CLASSIFICATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 920010.426C2
TELECOMMUNICATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 626-6031
INFORMATION FOR SEQ ID NO: 538:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-263-959-538/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-740-002-4
                                                                                                                                                                                                  US-09-263-959-538
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PRIOR FILLING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILLING DATE: 1995-06-07
NUMBER OF SED ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SED ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 538, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
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Best Local Similarity 80.0
Matches 28; Conservative
                                                                                                                                          Query Match
Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ROWEN, LEE
APPLICANT: KOOP, BED F
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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                                           26
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                                                                                                                  h 0.4%;
Similarity 96.0%;
24; Conservative
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Pred. No. 5.
                                                                                                                  Score 23.4; DB 10;
Pred. No. 4.6e+03;
D; Mismatches 1;
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TITLE OF INVENTION: SPECIFIC TO RSY F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR TILING DATE: 1995-06-18
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN PATENTINE SEQ ID NOS: 27
SEQ ID NO 2
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: U5/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
SEQ ID NO 1
CRGANISM: Artificial Sequence
PROURE: DATE 1995-06-07
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US-09-740-002-2/c
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US-09-740-002-1/c
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RESULT 9
                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Primer {\tt US-09-740-002-1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09740002 Patent No. US20020001798A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09740002
Patent No. US20020001798A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BRAMS, PE
APPLICANT: MORROW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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Best Local S
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APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUEACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                        255 GGCCAGGGCCCCCCCCTCTCTCTCTTTCTCTCTCTCT 289
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2; Mismatche
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Pred. No. 7.2e+03;
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                                                                                                                             DB 10;
9,3e+03;
7;
                                                                                                                                                                      Length 50;
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US-09-988-899-55/c
US-09-988-899-55/c
; Sequence 55, Application US/09988899
; Patent No. US20020102613A1
; GENERAL INFORMATION:
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US-09-988-899-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                 SOFTWARE: Pa
                                                                                                             CURRENT APPLICATION NUMBER: US/09/988,899
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: PCT/US00/13682
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 99201558.6
PRIOR PRIOR DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                 APPLICANT: HOOGENBOOM, HENDRICUS R.J.M.
TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
FILE REFERENCE: DX/003 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
CLASSIFICATION:
NAME: VELCCAL TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tent No.
              OTHER INFORMATION: Description of Artificial Sequence: Primer
                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        4416 AATAATAATAATAATAATAATAAT 4439
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS NUMBER OF SEQUENCES: 1279
                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: sin TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                        24 AATAATAATAATAATAATAAT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McMasters, David D
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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: Washington
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Koop, Ben !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09263959
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Pred. No. 8.
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US-09-853-526-272
                                                                                                                                                                    US-09-901-484A-272
                                                                                                                                                                                       RESULT 12
                                                                                                                                  Patent No. US2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele LOCATION: 1..47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
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NAME/KEY: primer_bind

LOCATION: 1.23
OTHER INFORMATION: potential microsequencing oligo 4-38-63.mis1
NAME/KEY: primer_bind

LOCATION: 25.47
OTHER INFORMATION: complement potential microsequencing oligo 4-38-63.mis2
US-09-853-526-272
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Thes 27; Conserva
                                                                                                                                                               GENERAL INFORMATION
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APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: Prostate Cancer Gene
FILE REFERENCE: GEN-TILIXC3D2
CURRENT APPLICATION NUMBER: US/09/901,484A
CURRENT FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 08/996,306
PRIOR FILING DATE: 1997-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cohen, Daniel APPLICANT: Blumenfeld,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/853,526
CURRENT FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CI
FILE REFERENCE: GENSET.18CP1CP
                                                                                                                    APPLICANT: Cohen, Daniel APPLICANT: Blumenfeld, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/218,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1998-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo Sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: base G ; A in SEQ ID195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: polymorphic fragment 4-38-63, variant version of SEQ ID195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2524 GTGACCGAGTCCTCTGGAAGTCTTATCCCCTGGTGCACGTGGT 2566
                                                                                                                                                                                                                                                                                                                             2144 AAGTGAAAAGAAACTCAGGCGAAACCAAAAACTATAT 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 GAGACTGGGTCAWCTGGATGTCAAGTGCACTGGTGGAGGCGGT 1
                                                                                                                                                                                                                                                                                                     4 AAGTTATAAGAAAATCAGGCGGAGGCTAAACTTTTT 39
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l similarity 67.4%;
29; Conservative
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                                                                                                   Chumakov, Ilya
                                                                                                                                                                                 Application US/09901484A
20020119460A1
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 2.2e+04
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                                                            Query Match
Best Local Similarity 69.0
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09845160 Patent No. US20020058045A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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SEQ ID NO 272
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP : PRIOR FILING DATE: 2000-05-31 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/845,160 CURRENT FILING DATE: 2001-05-01 PRIOR APPLICATION NUMBER: JP 2001-131688 PRIOR FILING DATE: 2001-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ADENOVIRUS VECTOR FILE REFERENCE: 081356/0163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MIZUGUCHI, HIROYUKI
APPLICANT: HAYAKAWA, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/853,526
                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide 7.
                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: primer_bind
LOCATION: (1).(23)
OTHER INFORMATION: potential microsequencing oligo 4-38-63.misl
NAME/KEY: primer_bind
LOCATION: (25)..(47)
OTHER INFORMATION: complement potential microsequencing oligo 4-38-63.mis2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US
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LOCATION: (24)..(24
OTHER INFORMATION:
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LOCATION: (1)..(47)
OTHER INFORMATION: polymorphic fragment 4-38-63, variant version of SEQ ID 195
                                                                                                                                                                                                                                                     ENGTH:
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                                   3922 CGCCGCGCCGCCGCTGCCAGTCAAGAGCCCGGCGGTGCTGC 3963
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CGCAGCGGCGCAGCCGCTCACGCAGCGGCCGTTGCAGC 42
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75.0%;
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Pred. No. 2.2e
0; Mismatches
                                                                      Score 21.2; DB 10
Pred. No. 2.6e+04;
0; Mismatches 13
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                                                                        Indels
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Search completed: March 12, Job time: 321 secs
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US-09-740-002-3/c
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Best Local S
Matches 26
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                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 44 LENGTH: 50
                                                                                                                                                      Matches
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Patent No. US20020001798A1
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/193,834
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brennan, Thomas J.
TITLE OF INVENTION: METHODS OF CREATING CONSTRUCTS USEFUL FOR INTRODUCING TITLE OF INVENTION: SEQUENCES INTO EMBRYONIC STEM CELLS
FILE REFERENCE: 376472000200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Klein, Robert D. APPLICANT: Brennan, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTII
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/087,523
CURRENT FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
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TYPE: DNA
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PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                       4323 CTCGCTCTTGGTACTTGGGACCCCAGTGCCTCGTTGAGGGCGCCA 4367
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Pred. No. 3.4e+04;
0; Mismatches 15
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Pred. No. 2.8e+04;
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length: 50
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Match
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5273
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12728.991 Million cell updates/sec
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 AV674036 AV674036
AV965544 AV965544
AZ42484 IM0203M14
AZ328467 IM0052E18
AV949200 AV949200
BJ001599 BJ001599
                                                                   Description
                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
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ORGANISM
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VERSION
KEYWORDS
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AV674036
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Elekaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Ent phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 49)

S Satch, N, Satou, Y, Kohara, Y, and Shin-i, T.

Expressed genes in Ciona intestinalis

L Unpublished (2000)

Contact: Nori Satch
Department of Zoology

Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Fax: 81-75-753-4081
Fax: 81-75-75-113

Email: satch@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                             AV674036 49 bp mRNA linear EST 05-OCT-2000 AV674036 Nor1 Satoh unpublished cDNA library Ciona intestinalis cDNA clone citb14a20 5', mRNA sequence.

AV674036 AV674036.1 GI:10112035
                                                                                                                                                                                                                                                                                                                              /organism-"Ciona intestinalis"
/db_xref-"taxon:7719"
/clone-"citbl420"
/clone_lib="Nori Satoh unpublished cDNA library"
                                                Location/Qualiflers
                                                                                                                                                                                                                                                                                                                              7 AZ5151B5
AI073810
AV672637
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AZ86483207

AIB13244

AV833587

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AZ8479185 1M0299J11
AV947640 AV947640
AZ8479185 1M0299J11
AV947640 AV947640
AZ8853064 2M0156N04
AZ8853064 AV833587 AV833587
AZ8649857 1M054500
AZ8439857 AV85350
AZ8439857 AV85350
AZ8439857 AV853454
AZ875459 AZ833442
AZ834546 AZ833442
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AZ85877 1M0054107
AZ515185 AZ85646
AZ87577 AZ85647
AZ85648 2M0102102
AZ85648 AZ857603.9
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                                                                                                                                                                         Enterogona;
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1M0082C0

Result

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Minimum DB Maximum DB

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RESULT 3
AZ424284
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AUTHORS
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AV965544
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Best Local Similarity
Matches 36; Conserv
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Best Local
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Mus musculus Eukaryota; Metazoa; Chordata; Eukaryota; Metazoa; Chordatia; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M.,
                                                                                                                    AZ424284 41 bp DNA linear GSS 03-OCT-200 1M0203M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0203M14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 49)
Satch, N., Satcu, Y., Kohara, Y. and Shin 1, T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ciona intestinalis.
                                                                                             AZ424284.1 GI:10548297
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Sakyo-ku, Kyoto, Kyoto 606-8502,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV965544.1 GI:19455240
                                                                     house mouse
                                                                                                                                                                                                                                                                    Similarity 78.36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       satoh@ascidian.zool.kyoto-u.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type-"whole animal"
/dev_stage="tailbud"
/note-"vector: Paluescript SK"
22 c 5 g 20 t
                                                                                                                                                                                                                                                                                                                                       /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                            /clone="cieg19i14"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                               /dev_stage-"egg"
                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Ciona intestinalis"
                                                                                                                                                                                                                                                                                   78.38;
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  Barber, M.,
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                                                                                                                                                                                                                                                                                 Score 30;
Pred. No.
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Pred. No. 1.3e+04;
0; Mismatches 10
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5 g 20 t
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                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
  Beacorn, T.,
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    Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                      Indels
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Unpublished (2000)
  Dunn,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                            Eukaryota;
Mammalia; E
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                                                                   louse mouse
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    Aoyagi, A., Barber, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
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                                                                                                GI:10388225
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266 CCCCCTCTCTCTTTCTCTCTCTCTCTCTCTCTTGCTTTGCTTTC 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0203 row: M column: 14
Seq primer: CACACAGGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 41.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                            AZ328467

AU DP DNA linear GSS 29
1M0052E18F Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0052E18 F, DNA sequence.
                    ikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murihae; Mus
(bases 1 to 40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Dear Maste **E. Coli strain XIIO-Gold, Tl-resistant, F-*
//lab hoste **E. Coli strain XIIO-Gold, Tl-resistant, F-*
//note **Vector: pwD42nv; purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 luch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance. "
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/clone="UUGC1M0203M14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
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M column: 14
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Pred. No. 1.3e
0; Mismatches
Beacorn, T., Duval, B., Hamil, C.,
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    AUTHORS
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32; Conser
                                                                                   Ciona intestinalis.
                                                                                                                                                                                AV949200 AV949200 Nori Satoh unpublished cDNA library, larva Ciona Intestinalis cDNA clone cilv02g12 5', mRNA sequence.
                    Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 47)
                                                                                                                                                                  intestinalis
AV949200
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                AV949200.1 GI:19437499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0052 row: E column: 18
Seq primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 40.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //lab_bost=E. Coll strain XL10-Gold, T1-resistant, F-*
//lab_bost=E. Coll strain XL10-Gold, T1-resistant, F-*
//loce="vector: PWDA27N; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligorucleotides were
ligated to the blunt ends in high mclar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gil
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (9114732114;pg)AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGCIM0052E18"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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/strain="C57BL/6J"
  Satou, Y., Kohara, Y. and Shin-i, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%;
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Pred. No. 1.5e+04;
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BJ001599
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(bases 1 to 44)

Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka, EST Project in Takeda's lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nor1 Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BJ001599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BJ001599 MF01SSA cDNA OTYZÍOS LATLÍPES CDNA CLONE MF01SSA009H08
                                                                                                                                                                                                                                                                                                                                                  Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japanese medaka.
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                                        Conservative
                                                                                                                                     /db_xref-"taxon:8090"
/clone='MFOLSSA009A08"
/clone_lib='MFOLSSA CDNA"
/sex-"mixture of female and male"
/tisue_type-"whole embryo"
/dev_stage="segmentation stage 20 -
dev_stage="segmentation stage 20 -
a 20 c 5 g 17 t
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/strain="Hd-rR"
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/db_xref="taxon:7719"
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                                                      0.6%;
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Pred. No. 1.8e+04;
                                                          Score 29.2;
Pred. No. 1
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                                        Mismatches
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                                                        DB 13; Length ..9e+04;
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FEATURES

Length 47;

Indels

0

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RESULT 5

FOCUS

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Query Match
Best Local Similarity
      268 CCCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmould, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: CACACAGGAAACAGCTATGACCClass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 49)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: F column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
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                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
/strain-"C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0146F20"
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                                                                                    0.6%;
                                                            <u>.</u>
                                                                                    Score 29.2; DB 17; Length 49; Pred. No. 2e+04;
                                                            Mismatches
                                                      8;
                                                            Indels
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Matches 31; Conserv
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0299 row: J column: 11
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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38 bp DNA linear GSS 04-OCT-200100299J11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic cione UUGC1M0299J11 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
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                                                            Conservative
                                                                                                                                                                                                                                                                                                /lab_bost="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_bost="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWM/A2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AFT139072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

18 c 1 g 19 t
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/clone="UUGC1M0299J11"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGClM library"
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                                                                                 0.5%;
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                                                                                    Score 28.6; DB 17
Pred. No. 2.6e+04;
                                                            Mismatches
                                                                                                                DB 17;
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                                                                                                                38;
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FEATURES

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BASE COUNT ORIGIN

JOURNAL COMMENT

REFERENCE AUTHORS

KEYWORDS SOURCE

GSS

ORGANISM

VERSION ACCESSION DEFINITION RESULT 7 AZ846608

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                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 38)
Dunn,D., Aoyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T. Expressed genes in Ciona intestinalis Unpublished (2000)
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Ciona intestinalis.
Ciona intestinalis
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                     house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ333216.1
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AZ333216

AZ333216

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AZ333216
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Nori Satoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV947640.1 GI:19425399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                satoh@ascidian.zool.kyoto-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="whole animal"
/dev_stage="young adult"
/note="vector: pBluescript SK"
23 c 0 g 23 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="ciad01g16"
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Pred. No. 2.8e+04;
0; Mismatches 10;
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AUTHORS
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VERSION
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AZ385990
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Best Local
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                   EUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sclurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
Le i (bases 1 to 47)
Le i (bases 1 to 47
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Tel: 801 585 5606
Fax: 801 585 7177
Fmail: ddunn@genet
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone UUGC1M0144D16 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                house mouse.
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nilarity 84.2%;
Conservative
308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agazose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4/32114]gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli xillo-Gold (Stratagene) cells and selected for ampicillin resistance.*
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0062N12"
/clone_lib="Mouse 10%b plasmld UUGC1M library"
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/strain="C57BL/6J"
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  E., SLC,
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KEYWORDS
SOURCE
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AZ853064
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VERSION
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                                                                 COMMENT
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Best Local Similarity 76.1
Matches 35; Conservative
                                                                                                                                TITLE
                                                                                                                                                                                                                  AUTHORS
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Location/Qualifiers
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Insert Length: 10000 Std Error: (
Plato: 0144 row: D column: 16
Seg primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
                                                                                                                                              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                        AZ853064 47 bp DNA linear GSS 21-FEB-200 2M0156K04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC2M0156K04 F, DNA sequence.
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                 plasmid inserts
Unpublished (2000)
                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 47)
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Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant,
/note="Vector: PWD42nv; Purified genomic DNA from !
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No. 3.1e+04;
0; Mismatches 11;
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AUTHORS
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AZ862836
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Best Local
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                     Contact: Robert B. University of Utah University of Utah
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Location/Qualifiers
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Insert Length: 10000 Std Error:
Plate: 0156 row K Column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Fax: 801 585 7177
                                                                                    Unpublished (2000)
                                                                                                           plasmid inserts
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Similarity 76.1%;
35; Conservative
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                                            Genome Center
                                                                 Weiss
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 47)
Dunn, B., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ862836 47 bp DNA linear GSS 21-FEB-200 2M0170N09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0170N09 R, DNA sequence.
308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polymered to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Laboratory Mouse DNA Resource
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/clone="UUGC2M0156K04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/note~"Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28.4; DB 17 Pred. No. 3.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
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AZ864870
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ORGANISM
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 bp DNA linear GSS 21-FEB-200 2M0174M10R Mouse 10kb plasmid UUGC1M library Nus musculus genomic clone UUGC2M0174M10 R, DNA sequence.
AZB64870
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0170 row: N column: 09
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                          SSD
                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ864870.1 GI:13064604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 0.5%;
Similarity 76.1%;
35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarsse gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gi)4732114;gb)Apr129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. "
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/db_xref="taxon:10090"
/clone="bugc2M0170N09"
/clone_lb="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 3.1e+04;
0; Mismatches 11;
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     S. 2030 E., SLC,
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DEFINITION
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AA773360
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Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
Washington Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.

WashD.NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA773360
49 bp mRNA linear EST 29-JAN-1998 ab65h08.sl Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:845727 3' similar to gb:X63657_rnal FOLLICULAR VARIANT TRANSLOCATION PROTEIN 1 PRECURSOR (HUMAN);, mRNA sequence. AA773360
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Insert Length: 10000 Std Error: (
Plate: 0174 row: M column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resources (documents/dnares). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orlice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gij4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.*
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/clone="UUGC2M0174M10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
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Pred. No. 3.1e+04;
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47; 0

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                                                                                               Ouery Match 0.5%;
Best Local Similarity 84.2%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                  source
                                                Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                          0
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/db_xref="taxon:9606"
                                                                                                 Score 28.4; DB 9;
Pred. No. 3.2e+04;
0; Mismatches 6;
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                                                                                                     Indels
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